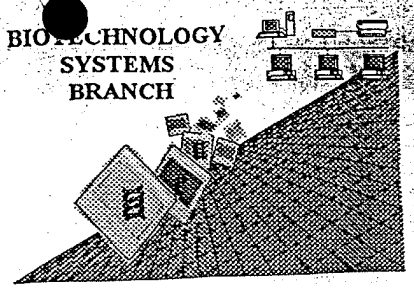
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/761,142

Source: OIPE

Date Processed by STIC: 1/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE JC154
JAN 30 2002
PATENT & TRADEMARK OFFICE

VERIFICATION SUMMARY DATE: 01/30/2001
PATENT APPLICATION: US/09/761,142 TIME: 11:19:35

Input Set : A:\31133A.ST25.txt
Output Set: N:\CRF3\01302001\I761142.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1221 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1221 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1221 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1221 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1221 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1285 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
M:340 Repeated in SeqNo=26
L:1286 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1286 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1286 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1286 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1287 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1287 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1287 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1287 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1839 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:1839 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:1839 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:1839 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
L:1839 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:11047 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:153
L:11047 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:153
L:11047 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:153
L:11047 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:153
L:11047 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:153
L:19618 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:258
L:19618 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:258
L:19618 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:258
L:19618 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:258
L:19618 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:258
L:28080 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:356
L:28080 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:356
L:28080 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:356
L:28080 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:356
L:28080 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:356

<210> 26
<211> 6413
<212> DNA
<213> Drosophila melanogaster

<400> 26
gaattccttc acaggcggtt tcttggccgc attatcgtta atattgttgt tggacatgta 60
cagctcgcat tgctgcacta ttttatccaa ttttcgaatt tcgctcagtt ccacgcaaga 120
tttgtgggac atttttaagt ctgcaaagta tagaaacgaa aaagtgttgc aaattataat 180
caaacattcg caaagctcag aatatccgga ttcgtaagca aattcaaata aatcttcgct 240
taaaaacaac ttaataataa atccaaaatt tccacttact ccagattgaa attggcgaaa 300
actgcgattt cttacctaat gcactttctt atttacttgc aaatcaaaac agaacaggta 360
tgacatgcac gcggagaaat caggagtgga aaatcatttt caatcaatta aaaacacttc 420
aattcgatct tgttcgttac acatactcta ctttttaaat atcatagata aaataaaaaa 480
atgaatagat gtatgtaaat acatggcatt ttcatttcga agtcaactgc tttataagac 540
caacttttt ttcccggtgt aatcaggctt tgcttttctg aaattttcag acatgcgtac 600
tgctttcggt tttcaaagat tcgaaaccac cgtgattttc gaaccattgt tattttcctt 660
ctcgcattcg gtcacactat tttcaaacgt aaacaattga tttttcctgc taaacaaaag 720
tggttgaaaa tgtcgggaat cgctgccaaa aagattgccg aagcggagga cctggtgaag 780
caggccgaga agaggtatcc ccaacaaaaa tatccttata aaggggtttc caaataacac 840
ccatctttat ttgcagcttg aagttgtcca tgctgaaatg ggttcctgat tacgatagtg 900
ctgcggatga gtattccaaa gctggtgagt ttcacaaagt aggagtgact aatatcaccc 960
agagtatcta tctataaaaa cattgtgaca tcaatgagat atgtaaatac tatgaattac 1020
agctaacgat tatcccaaag tatccataac ttgcaagata cacacatatt ggtgtacaat 1080
tatgtatctt tcttttacat ttttaattgc agccactgca tatcgaatag ctaaaagtta 1140
tgataagagc aaggagtgtt ttctgaaggc aatcgacgcc tataaaaaca acaagtcttg 1200
gttccatgct gcaaaggcat acgaacaggt gagcttaaat tgaagttaat ataagtgaag 1260
ttaataggaa atttaaaccc tctaaatgtg cacatcttct agatcatttt gctgtcaaag 1320
gatgccgata agctacacga agttgaggaa tacgccaaca aatcggcgag tttgtatcaa 1380
cagcacggtt ccccagaggc agccgcatcc gccttggata aagccgccaa gttaactgaa 1440
tccaagcatc ctgacatggc tttgcgcttc tatcagcatg ctctagaagt cataatggtt 1500
cgtcctattt gacactgctc tagtcaattc cattcttaaa ctattaattt tatacttacc 1560
cgacagatcg aggattccgt ccgtcaagca gccgagtatg atcaaaagtt tccaggatac 1620
tggtcaaact aaggaggtat gtacctatga ttgcaacgaa tcactttggg tatccttagc 1680
ttatatcatc caatcactcc aggtacgacg aagccacgaa tgcgctcaaa aaggagatca 1740
gcttgaatca gcaaacggaa tcttacggac aaattggacg cctagttgtg gccttggtga 1800
tggtccaact ggctcgcggg gattccgtgg aagccgaaaa gaccttcagg gagtggggaa 1860
actgctgcga gccagaggaa gtgtccacac tgcagaccct tctgcaagcc ttcgatgacg 1920
aggatcccga gttagctgct aggatgctgg catcccnatt catacgacat atggatgttg 1980
agtacgctat tctatctaaa aacattccac tacctcaggg tatacagatg gagaagaagg 2040
ctggcgacac tgctgctgtg agtattttta ttctaaaaat ggaatttgca atttttgttt 2100

→ see item 10 on Error Summary Sheet

(Partial listing of Sequence 26 - due to size of sequence, only first error shown - similar errors exist in the rest of the sequence)

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

RAW SEQUENCE LISTING DATE: 01/30/2001
PATENT APPLICATION: US/09/761,142 TIME: 11:19:34

Input Set : A:\31133A.ST25.txt
Output Set: N:\CRF3\01302001\I761142.raw

275 atttaccggg cgttaagacc caccgaatgc ggttaattta agtgataata taatatatta 420
276 aataagaata tgttaatacg tgtaccctgt gacaaatgtt tacagtctct aactaattcg 480
277 tactttcgta ttttacaaga acgtaaaacgt acgatatcag agtatctaaa agtaaaacca 540
278 cgaatcgttc atgtttacgg tttacggatt acgagtaaaa tggtatcaaa tcttttgatc 600
279 aactacctat cgaccatttac agactgacgg tttacattca actttttttac tgcgacatct 660
280 gcgattactt agcacgaaca taaataaata aaccgtgggg tcgtgatgtg cacgttaaat 720
281 aataaatttc acgaacagcg ccgtaatttt ataataatcc agtcatgttt tacatataaa 780
282 tctgaaactt cgaccgacta gttgctaaat tattcattga aagtggataa tttttattat 840
283 ttgggatttt gataatgcgg aatagccatc cacaatttat tattacgtaa ggtatatcga 900
284 tcaaggactt caagtatgcg tgttggaacc gttcattaaa taattcaata accccggtgt 960
285 gaaaatcaaa atcaaagatt gagacgctct ttctacaagc aagttcttct ttatctaatc 1020
286 cttcattaaa tcaggtatta aaaggaatca tgattcctga attgattgat aaaacaaagg 1080
287 gaaagcaagt ctgcacgttg cacaagaaga agaggacacc gcactggtgg accccaagcc 1140
288 ggcagaggca gatgccgtcg ataccccagcc gtgaaacgcc tcctcgtcaa aagcctcagc 1200
289 ggaaggaccc gtacatgcac cggaacttcc acagcatgtt cataaggtat atgcactcat 1260
290 ttgacgcaag tgttgacgtt cagtgtctga ttggaqaaac gtaagtcatg gattaaacgt 1320
291 caccggacca atatcggcgg gacccgagga tggagaagtg gaagtgccgc tacgccctcg 1380
292 tcgactaccc gtccaagctc ctcgcgtacg cgctggagaa gctcgctttc tgggtgtcgc 1440
293 tgctgtttcta cgtcggtcac gtgtcggaga agccgacgac gccgtaactc cctggcgtcc 1500
294 tgatggaagt cctcctcgtg ccgcgggacg ggtcgtcgac gacgatgcgg aagctgacga 1560
295 ggttcggccg cgtgcagatg ctcctccta cgaggtggtt ccgccatcga tgagactctt 1620
296 acgtccgcct cgagttgatg atgtcgacgt accgctagta acgggagctc cactctgtaa 1680
297 tttggtatgc gtcccatttt aagtgaacgg tgttcccatg aactcgtgtt cccatacaaa 1740
298 gccgtgcagc gaatacctic tcaataggtt attgaaaact taattgcgtg tgttgactga 1800
299 gtcacttgtg taaaattgat gaaaaaataa gcagtgcgaa tttatcttta gggacggttc 1860
300 tattctacac acaaaaaagt aagtttggta aaaacaatga tttcaaaaga aatttgattt 1920
301 atacagtttc cacgctagca atgataaata catgtgtcaa caactcgaaa acgaactaca 1980
302 atatttcaat atttcatcat tcctgcaatt ctgtcatttt ataaaaaaat tgtttcaagc 2040
303 gaacagataa gctaaagcta aggtatagtt ataatataat aatgttaaat acataaaaag 2100
304 tcaaaaaccc gaacaagtgg cgaatggtaa acccgttccg agcgttcata cggttttggt 2160
305 tctatttcct gctcctctgg gggtagttgc tgact 2195
308 <210> SEQ ID NO: 17
309 <211> LENGTH: 227
310 <212> TYPE: PRT
311 <213> ORGANISM: Drosophila melanogaster
313 <400> SEQUENCE: 17
314 Met Glu Lys Ser Phe Pro Ile Thr Pro Trp Lys Tyr Gly Leu Leu Val
315 1 5 10 15
317 Thr Cys Ile Leu Ile Val Thr Cys Asn Val Phe Phe Phe Ser Cys Gly
318 20 25 30
320 Val Thr Thr Trp Gly Ser Ala Val Ser Val Tyr Gly Ser Tyr Gly Ser
321 35 40 45
323 Ala Leu Cys Gly Gly Ala Val Phe Gly Val Ala Phe Leu Gly Met Tyr
324 50 55 60
326 Val Ala Leu Lys Val Ser Tyr Lys Tyr Ser Ile Tyr Tyr Leu Ile Cys
327 65 70 75 80
329 Ser Gly Leu Val Ile Ala Ala Leu Gly Ser Tyr Leu Phe Thr Phe Thr
330 85 90 95
332 Ala Met Arg Glu Gln Leu Met Gly Arg Phe Glu Glu Arg Met Arg Asp

RAW SEQUENCE LISTING DATE: 01/30/2001
PATENT APPLICATION: US/09/761,142 TIME: 11:19:34

Input Set : A:\31133A.ST25.txt
Output Set: N:\CRF3\01302001\I761142.raw

```
205 acgcggatct gcagcagacc cccgaccacc tctatctgga cgggtgcatc gaaaaggtgc 660
206 agagcttcta cgaaagcgac aagctgcgct tcatcatagt gtcctgggtg ctagtggcct 720
207 tcgagttaat ctgcttcgcc ttggccgtgt ttctggccat tagttttaag aacaagcagc 780
208 gacggatgga gttctagttc taggcttcgg taatctcgag ctatccaaca gtacaaactc 840
209 ggaatcgggg tctcgctgat atttttctct tcaacatttc ataaccaaat gcaaaggaca 900
210 gtcataaatt attcactcct accttaatgt aacctgtaat taaagtacat atttgtagtt 960
211 caattaccca ttataagtat cataataaat gtgcgcgtgt ttgttttcac atga       1014
214 <210> SEQ ID NO: 15
215 <211> LENGTH: 208
216 <212> TYPE: PRT
217 <213> ORGANISM: Drosophila melanogaster
219 <400> SEQUENCE: 15
220 Met Gly Cys Ala Thr Thr Ser Val Lys Ile Ala Ser Ile Val Leu Asn
221   1               5                  10                  15
223 Ala Val Leu Gly Phe Leu Ala Ala Gly Ala Ile Gly Trp Ile Ala Tyr
224              20                  25                  30
226 Asn Ala Asp Thr Glu Thr Glu Glu Phe Val Ile Ala Ala Tyr Ile Ala
227          35                  40                  45
229 Cys Ser Leu Ile Leu Val Phe Ala Leu Leu Gly Ile Phe Ala Ala Ile
230      50                  55                  60
232 Arg Glu Ser Val Val Leu Thr Ala Thr Ser Ala Val Phe Leu Leu Ile
233  65                  70                  75                  80
235 Leu Ala Ile Leu Gln Ile Val Ser Thr Cys Leu Phe Leu His Glu Phe
236                  85                  90                  95
238 Asp Val Lys Ser Gly Arg Asp Met Val Glu Val Ala Trp Gln Ala Asn
239             100                 105                 110
241 Asn Met Asp Ser Leu Gln Gln Lys His Glu Cys Cys Gly Gln Ser Ser
242         115                 120                 125
244 Ala Gln Asp Tyr Ile His Leu Ser Leu Leu Ile Pro Pro Ser Cys Tyr
245     130                 135                 140
247 Ala Asp Leu Gln Gln Thr Pro Asp His Leu Tyr Leu Asp Gly Cys Ile
248 145                 150                 155                 160
250 Glu Lys Val Gln Ser Phe Tyr Glu Ser Asp Lys Leu Arg Phe Ile Ile
251                 165                 170                 175
253 Val Ser Trp Val Leu Val Ala Phe Glu Leu Ile Cys Phe Ala Leu Ala
254             180                 185                 190
256 Val Phe Leu Ala Ile Ser Phe Lys Asn Lys Gln Arg Arg Met Glu Phe
257         195                 200                 205
263 <210> SEQ ID NO: 16
264 <211> LENGTH: 2195
265 <212> TYPE: DNA
266 <213> ORGANISM: Drosophila melanogaster
268 <400> SEQUENCE: 16
269 tacctcttca gcaaagggta ttgtgggacc ttcatgccgg atgaccagtg gacgtaagag 60
270 taacaccatt cacttttttct acgcgtaaag gggtaaggtc tcgaaagggt aaaagggctc 120
271 ggactgggtt taccccttaga acgtgttgtg ggccactacg ctcgttactc ggtttttagct 180
272 ttttagttat aacgcgggtt caagtgtaga aagcgttctc tcgtttttaa ccactgttac 240
273 tcggcgattt ctgatatttg tttagctacg ttagagtttt ttataaatat ttacgtatta 300
274 tggacaagtg tatgaatgta ttaaggcggc cggtcgacaa acattaaaaa cgttatagat 360
```

RAW SEQUENCE LISTING DATE: 01/30/2001
PATENT APPLICATION: US/09/761,142 TIME: 11:19:34

Input Set : A:\31133A.ST25.txt
Output Set: N:\CRF3\01302001\I761142.raw

<SEQ_ID_NO: 10>
<TYPE: DNA>
<ORGANISM: Artificial Sequence>
<FEATURE:>
<OTHER INFORMATION: Description of Artificial Sequence: PCR Primer Sequence Sp3>
<SEQUENCE: 10>
gagtacgcaa agctttaact atgt 24

<SEQ ID NO: 11>
<LENGTH: 23>
<TYPE: DNA>
<ORGANISM: Artificial Sequence>
<FEATURE:>
<OTHER INFORMATION: Description of Artificial Sequence: PCR Primer Sequence Sp6>
<SEQUENCE: 11>
tgaccacatc caaacatcct ctt 23

<SEQ ID NO: 12>
<LENGTH: 25>
<TYPE: DNA>
<ORGANISM: Artificial Sequence>
<FEATURE:>
<OTHER INFORMATION: Description of Artificial Sequence: PCR Primer Sequence Sp5>
<SEQUENCE: 12>
gcatcacaaa aatcgacgct caagt 25

<SEQ ID NO: 13>
<LENGTH: 19>
<TYPE: DNA>
<ORGANISM: Artificial Sequence>
<FEATURE:>
<OTHER INFORMATION: Description of Artificial Sequence: PCR Primer Sequence Spep1>
<SEQUENCE: 13>
gacactcaga atactattc 19

<SEQ ID NO: 14>
<LENGTH: 1014>
<TYPE: DNA>
<ORGANISM: Drosophila melanogaster>
<SEQUENCE: 14>
agcgaacgca gaacgcgcca gaccaaaaag ttcagattcg agagcggata tcccggcgag 60
cgttcacgga aatatatttg tttgttattc gagtccagca acgaatattt aaataaacaa 120
aaaacgaact ttattcgtgt gcggagagag aagtcaaaag atccaataaa atgggttgcg 180
ccacgaccag cgtgaagatc gcctccatcg ttctgaatgc cgttttaggg tttcttgctg 240
ctggggccat cggctggata gcttacaatg cggacacgga gacggaggaa ttcgtaatag 300
ccgcttacat cgcgtgctcg ctcatcctgg tctttgctct gctgggcatc ttcgcggcca 360
tccgggaatc ggtggtgctg actgcaacga gtgctgtctt cctgctgatc ttggccatcc 420
tgcagatcgt gagcacctgc ctgttcctcc acgagttcga cgtgaagagc ggccgggaca 480
tggtggaggt ggcctggcag gcgaacaaca tggattcctt gcagcagaag cacgagtgct 540
gcggccagag cagcgcccag gactatatcc acctcagcct gctgatcccg cccagctgct 600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001
TIME: 11:19:34

Input Set : A:\31133A.ST25.txt
Output Set: N:\CRF3\01302001\I761142.raw

68 <400> SEQUENCE: 4
69 ccttagcatg tccgtggggt ttgaat 26
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 28
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
79 Sequence Pry2
81 <400> SEQUENCE: 5
82 cttgccgacg ggaccacctt atgttatt 28
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 19
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
92 Sequence Plw3-1
94 <400> SEQUENCE: 6
95 tgtcggcgtc atcaactcc 19
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 29
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
105 Sequence Pwht1
107 <400> SEQUENCE: 7
108 gtaacgctaa tcactccgaa caggtcaca 29
111 <210> SEQ ID NO: 8
112 <211> LENGTH: 25
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
118 Sequence Splac2
120 <400> SEQUENCE: 8
121 gaattcactg gccgtcgttt tacaa 25
124 <210> SEQ ID NO: 9
125 <211> LENGTH: 22
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
131 Sequence Sp1
133 <400> SEQUENCE: 9
134 acacaacctt tcctctcaac aa 22
137 <210> SEQ ID NO: 10
138 <211> LENGTH: 24

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001
TIME: 11:19:34

Input Set : A:\31133A.ST25.txt
Output Set: N:\CRF3\01302001\I761142.raw

Does Not Comply
Corrected Diskette Needed
P 6

```
 3 <110> APPLICANT: Kamdar, Kim
 4       Broadus, Julie
 5       Stam, Lynn
 6       Bachmann, Jane
 8 <120> TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
 9       PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
11 <130> FILE REFERENCE: PB/5-31133A
13 <140> CURRENT APPLICATION NUMBER: US/09/761,142
13 <141> CURRENT FILING DATE: 2001-01-16
13 <150> PRIOR APPLICATION NUMBER: US 60/176,418
14 <151> PRIOR FILING DATE: 2000-01-14
16 <160> NUMBER OF SEQ ID NOS: 361
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 27
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
27       Sequence Plac4
29 <400> SEQUENCE: 1
30 actgtgcgtt aggtcctgtt cattgtt                                        27
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 24
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
40       Sequence Plac1
42 <400> SEQUENCE: 2
43 cacccaaggc tctgctccca caat                                          24
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 23
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
53       Sequence Pry4
55 <400> SEQUENCE: 3
56 caatcatatc gctgtctcac tca                                           23
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 26
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
66       Sequence Pry1
```

OIPE JC154 JAN 30 2002 PATENT & TRADEMARK OFFICE

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/761,142

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.